

**Figure S1** TEM images of MPA-modified CdTe QDs and its corresponding size distribution for 2.2 nm (a,b) and 3.5 nm (c,d).

**Abbreviations:** TEM, transmission electron microscopy; MPA, 3-mercaptopropionic acid; QDs, quantum dots.



Figure S2 Dynamic light scattering (A and B) and  $\xi$ -potential measurements (C and D) of 3.5 nm and 2.2 nm MPA-modified CdTe QDs. DLS values are the average of at least 10 runs each containing 15 submeasurements.  $\xi$ -potential values are the average of at least 10 runs each containing 30 submeasurements.



Figure S3 UV-vis absorption (a) and PL spectra (b) of MPA-modified CdTe QDs (2.2 nm and 3.5 nm). The inset shows the fluorescent photograph of as-synthesized CdTe QDs under UV irradiation.



Figure S4. The uptake of MPA-modified CdTe QDs by the hippocampal neurons of

treated rats. The arrow indicates accumulated QDs in the lysosome.



Figure S5. TEM images of hippocampus of rats treated with 400  $\mu\text{g/mL}$  and 800

 $\mu g/mL$  2.2 nm and 3.5 nm MPA-modified CdTe QDs.

Table S1. All GO terms of genes differentially expressed during 2.2 nm and 3.5 nm

Category	Term	No. of gene	Count( %)	Fold Enrich-	Bonferroni corrected
2 2 nm CdTe (	D vs. Control			ment	Pvalue
Z.2 IIII Cure C					
Biological	immune response	10	25	10.07	7.78E-05
Biological					
Process	response to virus	5	12.5	45.32	1.19E-03
Cellular					
Component	integrin complex	3	7.5	80.82	1.64E-02
3.5 nm CdTe OD vs. Control					
Biological					
Process	immune response	107	15.20	6.69	8.33E-56
Biological					
Process	defense response	83	11.79	5.39	3.10E-34
Biological	response to organic	=0	10.25	2	
Process	substance	73	10.37	2.04	1.69E-05
Biological	1.	71	10.00	4.2.4	1.445.00
Process	response to wounding	/1	10.09	4.34	1.44E-22
Biological	regulation of cell	50	۶ <b>٦</b> 4	2.26	2 55E 05
Process	proliferation	50	0.24	2.20	2.33E-03
Biological	positive regulation of	57	8 10	636	4 12E-26
Process	immune system process	51	0.10	0.50	4.12L-20
Biological	regulation of programmed	55	7 81	2.08	1.07E-03
Process	cell death	55	7.01	2.00	1.0712 05
Biological	regulation of cell death	55	7.81	2.07	1.22E-03
Process					
Biological	regulation of apoptosis	54	7.67	2.07	1.65E-03
Process					
Biological	inflammatory response	51	7.24	6.09	5.10E-22
Process					
Biological	positive regulation of	51	7.24	5.69	1.30E-20
Process	response to stimulus				
Biological	cell activation	50	7.10	5.35	6.86E-19
Process					
Biological	leukocyte activation	43	6.11	5.23	2.18E-15
Process Biologics1	positivo rogulation of				
Process	molecular function	42	5.97	2.14	1.51E-02

MPA-modified CdTe QD exposure on rat hippocampus.

Biological	positive regulation of	40	5 68	7 35	9 80E-20
Process	immune response		0.00	1.00	<i></i>
Biological	positive regulation of cell	39	5 54	2.60	3 18E-04
Process	proliferation	57	0.01	2.00	5.101 01
Biological	response to bacterium	36	5 11	4 40	6 14E-10
Process		50	0.11	1.10	0.1112 10
Biological	immune effector process	35	4 97	7 49	3 80E-17
Process	minute effector process	55	1.97	7.19	5.00E 17
Biological	regulation of cell activation	35	4 97	5 39	2 47F-12
Process	regulation of cell activation	55	ч.ут	5.57	2.4712-12
Biological	regulation of leukocyte	33	4 69	5 31	3 18F-11
Process	activation	55	ч.0 <i>)</i>	5.51	J.10L-11
Biological	positive regulation of	31	4.40	2.58	0.60E-03
Process	developmental process	51	7.70	2.50	).0)L-03
Biological	positive regulation of cell	30	1 26	2 43	1 63E 02
Process	communication	50	4.20	2.45	4.0512-02
Biological	innata immuna racnonca	20	4 1 2	0 02	070E16
Process	milate milliture response	29	4.12	0.05	0.70L-10
Biological	lumphoaute activition	20	4 1 2	1 17	1 21E 07
Process	Tymphocyte activation	29	4.12	4.47	1.5112-07
Biological	locomotory babayior	20	4.12	3 61	2 00E 05
Process	locomotory benavior	29	4.12	5.01	2.001-05
Biological	hemopoietic or lymphoid	20	4 1 2	2 00	1.07E.02
Process	organ development	29	4.12	3.00	1.0/E-03
Biological	immune system	20	4 1 2	2 87	2 79E 02
Process	development	29	4.12	2.07	2.781-05
Biological	positive regulation of signal	28	2.08	2.54	4 10E 02
Process	transduction	20	5.70	2.34	4.1012-02
Biological	toxic	27	2.84	8 17	6 04E 14
Process	taxis	21	5.84	0.42	0.941-14
Biological	chamatavis	27	2.84	8 17	6 04E 14
Process	chemotaxis	21	5.84	0.42	0.941-14
Biological	activation of immune	27	2.84	רר ר	6 18E 13
Process	response	21	5.84	1.11	0.161-15
Biological	positive regulation of cell	27	2.84	636	1 <i>4</i> 1E 10
Process	activation	21	5.84	0.30	1.4112-10
Biological	regulation of lymphocyte	27	2.94	1 95	1 02E 07
Process	activation	21	5.04	4.65	1.03E-07
Biological	hamonoiasis	27	2.94	2.00	1.66E.02
Process	hemopolesis	21	5.04	3.09	1.00E-03
Biological	response to molecule of	26	2.60	5.06	1 125 00
Process	bacterial origin	20	3.09	3.20	4.13E-08
Biological	regulation of protein kinase	26	2.60	276	2 225 02
Drogoss	cascade	20	3.69	2.76	2.22E-02

Biological Process	positive regulation of multicellular organismal process	26	3.69	2.70	3.16E-02
Biological Process	positive regulation of cell differentiation	26	3.69	2.67	3.87E-02
Biological Process	leukocyte mediated immunity	25	3.55	8.63	6.18E-13
Biological Process	positive regulation of leukocyte activation	25	3.55	6.11	3.70E-09
Biological Process	regulation of cytokine production	25	3.55	4.18	1.50E-05
Biological Process	regulation of response to external stimulus	25	3.55	4.02	3.23E-05
Biological Process	regulation of immune effector process	24	3.41	5.70	5.17E-08
Biological Process	response to lipopolysaccharide	24	3.41	5.31	2.38E-07
Biological Process	adaptive immune response	23	3.27	9.02	4.94E-12
Biological Process	based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	23	3.27	9.02	4.94E-12
Biological Process	regulation of T cell activation	23	3.27	5.32	6.25E-07
Biological Process	wound healing	23	3.27	3.42	2.50E-03
Biological Process	antigen processing and presentation	22	3.13	6.86	9.60E-09
Biological Process	positive regulation of lymphocyte activation	22	3.13	5.87	2.37E-07
Biological Process	T cell activation	22	3.13	5.09	3.96E-06
Biological Process	positive regulation of protein kinase cascade	21	2.98	3.20	2.35E-02
Biological Process	lymphocyte mediated immunity	20	2.84	8.49	1.74E-09
Biological Process	aging	20	2.84	3.45	1.34E-02
Biological Process	myeloid leukocyte activation	19	2.70	9.28	1.31E-09

Biological	acute inflammatory	10	2 70	5 47	2.05E.05
Process	response	19	2.70	5.47	2.0512-05
Biological	immune response-activating	18	2.56	8 17	3 35E-08
Process	signal transduction	10	2.50	0.47	5.551-08
Biological Process	leukocyte migration	18	2.56	8.18	6.39E-08
Dielegiaal	immune response-				
Diological	regulating signal	18	2.56	7.77	1.59E-07
Process	transduction				
Dielogical	antigen processing and				
Diological	presentation of peptide	17	2.41	11.29	8.51E-10
FIOCESS	antigen				
Biological	positive regulation of	17	2.41	6 57	0.25E.06
Process	defense response	17	2.41	0.37	9.55E-00
Biological	positive regulation of T cell	17	2 41	6.02	2.540.05
Process	activation	17	2.41	0.03	3.34E-03
Biological	regulation of leukocyte	17	2 41	5.05	A 26E 05
Process	mediated immunity	17	2.41	5.95	4.30E-03
Biological	positive regulation of	17	2.41	5 07	5 25 - 05
Process	cytokine production	17	2.41	5.87	5.55E-05
Biological	call chamatavis	16	2 27	10.36	2 27E 08
Process	cell chemotaxis	10	2.21	10.50	2.2712-08
Biological	regulation of lymphocyte	16	2 27	4 71	2 25E 02
Process	proliferation	10	2.21	4./1	5.25E-05
Biological	regulation of mononuclear	16	2 27	1 65	3 77E 03
Process	cell proliferation	10	2.27	4.05	5.7712-05
Biological	regulation of leukocyte	16	2 27	4 55	5.04E-03
Process	proliferation	10	2.21	4.55	5.041-05
Biological	leukocyte chemotavis	15	2 13	10.50	0 80F-08
Process	leukoeyte enemotaxis	15	2.15	10.50	).0)E 00
Biological	cell activation during	15	2 13	9.03	1.03E-06
Process	immune response	15	2.13	2.05	1.051-00
Biological	leukocyte activation during	15	2 13	9.03	1.03E-06
Process	immune response	15	2.15	2.05	1.052.00
Biological	immunoglobulin mediated	15	2 13	8 09	5 29E-06
Process	immune response	15	2.15	0.09	5.271 00
Biological	cytokine production	15	2.13	7 93	7 15E-06
Process	cytokine production	15	2.15	1.95	7.1012 00
Biological	B cell mediated immunity	15	2 13	7 77	9 58E-06
Process	D con moduled minuney	15	2.15	1.11	).50E 00
Biological	regulation of innate	15	2 13	7 62	1 27F-05
Process	immune response	10	2.13	1.02	1.2712-03
Biological	negative regulation of	15	2.13	4 62	9 70E-03
Process	immune system process	15	2.13	1.02	2.101-03

Biological Process	defense response to bacterium	15	2.13	4.18	3.26E-02
Biological	response to virus	14	1.99	7.88	3.10E-05
Biological	regulation of adaptive	14	1.99	5.75	1.75E-03
Process	regulation of adaptive				
Dislosissi	immune response based on				
Process	immune receptors built	14	1.99	5.75	1.75E-03
	from immunoglobulin superfamily domains				
Biological	immune response-activating	10	1.05	0.01	1.005.04
Process	cell surface receptor signaling pathway	13	1.85	8.01	1.00E-04
Biological	immune response-				
Process	regulating cell surface receptor signaling pathway	13	1.85	7.32	3.06E-04
Biological	positive regulation of	13	1 85	6 60	1 05E-03
Process	immune effector process	15	1.00	0.00	1.001 00
Biological Process	regulation of lymphocyte mediated immunity	13	1.85	5.18	1.61E-02
Biological	regulation of lymphocyte	12	1 70	5 4 5	2 52E_02
Process	differentiation	12	1.70	5.75	2.321-02
Biological	positive regulation of	12	1 70	5 27	3 54E-02
Process	lymphocyte proliferation		1.70	0.27	0.012 02
Biological	mononuclear cell	12	1.70	5.18	4.18E-02
Process	proliferation				
Biological	antigen processing and				
Process	presentation of exogenous peptide antigen	11	1.56	14.24	2.39E-06
Biological	antigen processing and				
Process	presentation of exogenous antigen	11	1.56	11.39	3.55E-05
Biological	positive regulation of	11	156	7.01	1 995 02
Process	lymphocyte differentiation	11	1.30	/.91	1.88E-03
Biological	leukocyte proliferation	11	1 56	6 62	1 11E-02
Process	leukoeyte promeration	11	1.50	0.02	1.1112 02
Biological	mononuclear cell	11	1.56	6.62	1.11E-02
Process Biological	promeration				
Process	neutrophil chemotaxis	10	1.42	11.26	2.44E-04

Biological Process	myeloid cell activation during immune response	10	1.42	9.96	8.40E-04
Biological Process	positive regulation of T cell differentiation	10	1.42	7.62	1.07E-02
Biological	antigen receptor-mediated	10	1.42	7.40	1.38E-02
Biological	positive regulation of innate				
Process	immune response	10	1.42	6.81	2.86E-02
Biological	positive regulation of				
Process	adaptive immune response	10	1.42	6.64	3.58E-02
	positive regulation of				
	adaptive immune response				
Riological	based on somatic				
Biological	recombination of immune	10	1.42	6.64	3.58E-02
FIOCESS	receptors built from				
	immunoglobulin				
	superfamily domains				
	antigen processing and				
Biological	presentation of exogenous	9	1.28	16.65	3.12E-05
Process	peptide antigen via MHC				
	class II				
Biological	antigen processing and	_			
Process	presentation of peptide	9	1.28	16.65	3.12E-05
	antigen via MHC class II				
D' 1 ' 1	antigen processing and				
Biological	presentation of peptide or	9	1.28	14.56	1.25E-04
Process	polysaccharide antigen via				
	MHC class II				
Process	T cell proliferation	9	1.28	7.77	3.46E-02
Biological	regulation of acute	9	1 28	7 52	4 49E-02
Process	inflammatory response	-	1.20	,	
Biological	leukocyte adhesion	8	1.14	9.01	4.69E-02
Process	5				
Biological	B cell receptor signaling	7	0.99	13.94	1.19E-02
Process	pathway				
Biological	positive regulation of tumor	7	0.99	13.94	1.19E-02
Process	necrosis factor production				
Cellular	plasma membrane	160	22.73	1.71	3.40E-11
Component					
Companyat	extracellular region	99	14.06	1.98	5.15E-09
Collular					
Component	plasma membrane part	91	12.93	1.72	5.57E-05

Cellular		62	۹ <u>۵</u> ۶	2.22	1 42E 07
Component	extracentular region part	03	8.95	2.33	1.43E-07
Cellular	autro collulor crosso	10	6.07	2.50	2.065.06
Component	extracentilar space	48	0.82	2.30	3.00E-00
Cellular	coll avefoco	20	5 5 1	2.04	1 205 06
Component	cen surface	39	5.54	2.94	1.20E-00
Cellular	external side of plasma	27	2.04	4 1 4	1 <b>27</b> E 07
Component	membrane	21	3.84	4.14	4.2/E-0/
Cellular		26	2.60	2 20	5.925.05
Component	vacuole	26	3.69	5.38	5.82E-05
Cellular	1	25	2.55	2.05	5 105 07
Component	lysosome	25	3.55	3.95	5.10E-06
Cellular	1.2. 1	25	2.55	2.05	5 10E 0C
Component	lytic vacuole	25	3.55	3.95	5.10E-06
Cellular		1.5	0.10	2.66	1 7 45 00
Component	receptor complex	15	2.13	3.66	1.74E-02
Cellular			1.54	<b>5</b> 0 <b>7</b>	
Component	vesicle lumen	11	1.56	5.87	4.08E-03
Cellular			1.54	5.01	
Component	platelet alpha granule	11	1.56	5.31	1.02E-02
Cellular					
Component	MHC protein complex	11	1.56	5.21	1.21E-02
Cellular	platelet alpha granule	10		<i>.</i>	
Component	lumen	10	1.42	6.40	5.76E-03
Cellular	cytoplasmic membrane-				
Component	bounded vesicle lumen	10	1.42	5.95	1.07E-02
Cellular					
Component	T cell receptor complex	6	0.85	13.96	1.08E-02
Cellular	alpha-beta T cell receptor	_			
Component	complex	5	0.71	21.33	1.04E-02
Molecular	protein dimerization				
Function	1				
1 unction	activity	42	5.97	2.11	5.13E-03
Molecular	activity	42	5.97	2.11	5.13E-03
Molecular Function	activity carbohydrate binding	42 34	5.97 4.83	2.11 2.68	5.13E-03 3.00E-04
Molecular Function Molecular	activity carbohydrate binding	42 34	5.97 4.83	2.11 2.68	5.13E-03 3.00E-04
Molecular Function Molecular Function	activity carbohydrate binding cytokine binding	42 34 21	5.97 4.83 2.98	<ul><li>2.11</li><li>2.68</li><li>6.42</li></ul>	5.13E-03 3.00E-04 3.19E-08
Molecular Function Molecular Function Molecular	activity carbohydrate binding cytokine binding	42 34 21	<ul><li>5.97</li><li>4.83</li><li>2.98</li></ul>	<ul><li>2.11</li><li>2.68</li><li>6.42</li></ul>	5.13E-03 3.00E-04 3.19E-08
Molecular Function Molecular Function Molecular Function	activity carbohydrate binding cytokine binding cytokine activity	42 34 21 19	<ul><li>5.97</li><li>4.83</li><li>2.98</li><li>2.70</li></ul>	<ul><li>2.11</li><li>2.68</li><li>6.42</li><li>4.59</li></ul>	5.13E-03 3.00E-04 3.19E-08 8.69E-05
Molecular Function Molecular Function Molecular Function Molecular	activity carbohydrate binding cytokine binding cytokine activity	42 34 21 19	<ul><li>5.97</li><li>4.83</li><li>2.98</li><li>2.70</li></ul>	<ul><li>2.11</li><li>2.68</li><li>6.42</li><li>4.59</li></ul>	5.13E-03 3.00E-04 3.19E-08 8.69E-05
Molecular Function Molecular Function Molecular Function Molecular Function	activity carbohydrate binding cytokine binding cytokine activity polysaccharide binding	42 34 21 19 17	<ul><li>5.97</li><li>4.83</li><li>2.98</li><li>2.70</li><li>2.41</li></ul>	<ul><li>2.11</li><li>2.68</li><li>6.42</li><li>4.59</li><li>3.90</li></ul>	5.13E-03 3.00E-04 3.19E-08 8.69E-05 4.42E-03
Molecular Function Molecular Function Molecular Function Molecular Function Molecular	activity carbohydrate binding cytokine binding cytokine activity polysaccharide binding	42 34 21 19 17	<ul><li>5.97</li><li>4.83</li><li>2.98</li><li>2.70</li><li>2.41</li></ul>	<ul><li>2.11</li><li>2.68</li><li>6.42</li><li>4.59</li><li>3.90</li></ul>	5.13E-03 3.00E-04 3.19E-08 8.69E-05 4.42E-03
Molecular Function Molecular Function Molecular Function Molecular Function Molecular Function	activity carbohydrate binding cytokine binding cytokine activity polysaccharide binding pattern binding	42 34 21 19 17 17	<ul> <li>5.97</li> <li>4.83</li> <li>2.98</li> <li>2.70</li> <li>2.41</li> <li>2.41</li> </ul>	<ul> <li>2.11</li> <li>2.68</li> <li>6.42</li> <li>4.59</li> <li>3.90</li> <li>3.90</li> </ul>	5.13E-03 3.00E-04 3.19E-08 8.69E-05 4.42E-03 4.42E-03
Molecular Function Molecular Function Molecular Function Molecular Function Molecular Function Molecular	activity carbohydrate binding cytokine binding cytokine activity polysaccharide binding pattern binding	42 34 21 19 17 17	<ul> <li>5.97</li> <li>4.83</li> <li>2.98</li> <li>2.70</li> <li>2.41</li> <li>2.41</li> </ul>	<ul> <li>2.11</li> <li>2.68</li> <li>6.42</li> <li>4.59</li> <li>3.90</li> <li>3.90</li> </ul>	5.13E-03 3.00E-04 3.19E-08 8.69E-05 4.42E-03 4.42E-03

Molecular Function	chemokine activity	14	1.99	11.63	3.04E-08
Molecular Function	chemokine receptor binding	14	1.99	11.28	4.84E-08
Molecular Function	heparin binding	13	1.85	4.80	9.05E-03

Table S2. The rest of differentially expressed pathways in the control with 3.5 nm

Torres	Pathway	Input number	Background	Corrected
lerm	ID	of gene	number of gene	<b>P-Value</b>
Chemokine signaling pathway	rno04062	31	155	0.000224868
Legionellosis	rno05134	16	50	0.000245244
Hematopoietic cell lineage	rno04640	20	76	0.000245244
Phagosome	rno04145	31	158	0.000245244
Herpes simplex infection	rno05168	33	176	0.00027901
Viral myocarditis	rno05416	19	72	0.000307548
Rheumatoid arthritis	rno05323	20	79	0.000307548
NOD-like receptor signaling pathway	rno04621	16	54	0.0003588
Primary immunodeficiency	rno05340	13	36	0.0003588
Graft-versus-host disease	rno05332	15	48	0.0003588
Complement and coagulation cascades	rno04610	17	62	0.000426855
NF-kappa B signaling pathway	rno04064	20	83	0.000432465
Influenza A	rno05164	28	151	0.000885282
Type I diabetes mellitus	rno04940	15	57	0.001523512
Allograft rejection	rno05330	14	52	0.001953369
Natural killer cell mediated cytotoxicity	rno04650	18	81	0.002039337
HTLV-I infection	rno05166	38	250	0.002039337
Autoimmune thyroid disease	rno05320	14	56	0.00331383
TNF signaling pathway	rno04668	19	98	0.005508827
Cytosolic DNA-sensing pathway	rno04623	12	46	0.00566281
Malaria	rno05144	12	47	0.006431329
Salmonella infection	rno05132	15	72	0.009330565
Fc gamma R-mediated phagocytosis	rno04666	15	76	0.014354617
Inflammatory bowel disease (IBD)	rno05321	12	54	0.016114137
Leukocyte transendothelial migration	rno04670	18	103	0.017024126
Measles	rno05162	19	116	0.024163724
T cell receptor signaling pathway	rno04660	17	99	0.024288879
B cell receptor signaling pathway	rno04662	13	67	0.026966697
Epstein-Barr virus infection	rno05169	26	191	0.044440886

MPA-modified CdTe QD-treatment.

Intestinal immune network for IgA	rno0/1672	0	41	0.048359461
production	111004072	)	41	0.040339401